10048024 Results

SEQ ID NO: 1

RESULT 16
AAW84306
ID AAW84306 standard; peptide; 27 AA.
XX
AC AAW84306;
XX
DT 18-MAR-1999 (first entry)
XX
DE Finger 3 of a NABP specific for a G12V mutant ras oncogene.
XX
KW Zinc finger; nucleic acid binding protein; NABP; ras oncogene mutant;
KW Cys2-His2 zinc finger; detection; gene therapy; gene delivery.
XX
OS Synthetic.
XX
PN WO9853059-A1.
XX
PD 26-NOV-1998.
XX
PF 26-MAY-1998; 98WO-GB001514.
XX
PR 23-MAY-1997; 97GB-00010807.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PI Choo Y, Klug A, Isalan M;
XX
DR WPI; 1999-045308/04.
XX
PT Preparation of nucleic acid binding proteins - by designing protein
PT sequences of a Cys2-His2 zinc finger class based on a nucleic acid base
PT triplet in a target nucleic acid sequence.
XX
PS Example 4; Fig 5C; 62pp; English.
XX
CC The present sequence represents finger 1 of a nucleic acid binding
CC protein (NABP) specific for a G12V mutant ras oncogene. The specification
CC describes a method for preparing a NABP of the Cys2-His2 zinc finger
CC class capable of binding to a nucleic acid base triplet in a target
CC nucleic acid sequence. Binding to the 5' base of the triplet by an alpha-
CC helical zinc finger nucleic acid binding motif in the protein is
CC determined as follows: (a) if the 5' base in the triplet is A, then
CC position +6 in the alpha -helix is Glu, Asn or Val; (b) if the 5' base in
CC the triplet is C, then position +6 in the alpha-helix is Ser, Thr, Val,
CC Ala, Glu or Asn. The methods can be used for designing a protein which is
CC capable of binding to any predefined nucleic acid sequence. The NABPs can
CC be used for the detection of target nucleic acid molecules. They can also
CC be used in gene therapy, e.g. for the delivery of functional genes into
CC defective genes, or the delivery of nonsense nucleic acid to disrupt
CC undesired nucleic acid
XX
SQ Sequence 27 AA;

  Query Match   4.2%; Score 7; DB 2; Length 27;
  Best Local Similarity   100.0%; Pred. No. 12;
  Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   109 HTRTHTG 115
              |||||||
Db   19 HTRTHTG 25

RESULT 17
AAW78389
ID AAW78389 standard; peptide; 27 AA.
XX
AC AAW78389;

XX
DT 11-MAY-1999 (first entry)
XX
DE Finger #3 of zinc finger targeted to mutant H-ras coding sequence.
XX
KW Zinc finger; target sequence; binding assay; mutant;
KW phosphorylation site; functional domain.
XX
OS Synthetic.
XX
PN WO9853060-A1.
XX
PD 26-NOV-1998.
XX
PF 26-MAY-1998; 98WO-GB001516.
XX
PR 23-MAY-1997; 97GB-00010809.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PI Choo Y, Klug A, Isalan M;
XX
DR WPI; 1999-045309/04.
XX
PT Rules for designing zinc finger nucleic acid binding proteins specific
PT for any base quadruplet - relate bases in the quadruplet to specific
PT amino acids in the alpha-helical binding motif, used to detect target
PT nucleic acids, e.g. for identification of mutants and phosphorylation
PT sites.
XX
PS Example 1; Fig 1C; 57pp; English.
XX
CC This sequence represents finger #3 from a synthesised zinc finger
CC targeted to the mutant coding sequence for amino acids 8-16 of the H-ras
CC oncogene (AAX16975). The synthesised zinc finger belongs to the Cys2-His2
CC zinc finger (ZF) class (AAW78382). The ZF are generated so that they able
CC to bind a nucleic acid quadruplet in a target sequence, where binding to
CC base 4 of the quadruplet by an alpha-helical ZF binding motif is
CC determined as: (a) if base 4 is A, then position +6 in the helix is Gln
CC and position ++2 is not Asp (++2 indicates a residue present in an
CC adjacent, C-terminal ZF) and (b) if base 4 is C, then position +6 may be
CC any residue provided ++2 is not Asp. The ZF are used to detect target
CC nucleic acids in a binding assay, e.g. for identification of mutants
CC (they can differentiate between single bp changes in the target) or
CC potential phosphorylation sites, and to characterise functional domains
CC of a protein
XX
SQ Sequence 27 AA;

Query Match 4.2%; Score 7; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        109 HTRTHTG 115
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Db         19 HTRTHTG 25
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RESULT 18
AAW84305
ID AAW84305 standard; peptide; 28 AA.
XX
AC AAW84305;
XX
DT 18-MAR-1999 (first entry)
XX
DE Finger 2 of a NABP specific for a G12V mutant ras oncogene.
XX
KW Zinc finger; nucleic acid binding protein; NABP; ras oncogene mutant;
KW Cys2-His2 zinc finger; detection; gene therapy; gene delivery.
XX

OS Synthetic.
XX
PN WO9853059-A1.
XX
PD 26-NOV-1998.
XX
PF 26-MAY-1998; 98WO-GB001514.
XX
PR 23-MAY-1997; 97GB-00010807.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PI Choo Y, Klug A, Isalan M;
XX
DR WPI; 1999-045308/04.
XX
PT Preparation of nucleic acid binding proteins - by designing protein
PT sequences of a Cys2-His2 zinc finger class based on a nucleic acid base
PT triplet in a target nucleic acid sequence.
XX
PS Example 4; Fig 5C; 62pp; English.
XX
CC The present sequence represents finger 1 of a nucleic acid binding
CC protein (NABP) specific for a G12V mutant ras oncogene. The specification
CC describes a method for preparing a NABP of the Cys2-His2 zinc finger
CC class capable of binding to a nucleic acid base triplet in a target
CC nucleic acid sequence. Binding to the 5' base of the triplet by an alpha-
CC helical zinc finger nucleic acid binding motif in the protein is
CC determined as follows: (a) if the 5' base in the triplet is A, then
CC position +6 in the alpha -helix is Glu, Asn or Val; (b) if the 5' base in
CC the triplet is C, then position +6 in the alpha-helix is Ser, Thr, Val,
CC Ala, Glu or Asn. The methods can be used for designing a protein which is
CC capable of binding to any predefined nucleic acid sequence. The NABPs can
CC be used for the detection of target nucleic acid molecules. They can also
CC be used in gene therapy, e.g. for the delivery of functional genes into
CC defective genes, or the delivery of nonsense nucleic acid to disrupt
CC undesired nucleic acid
XX
SQ Sequence 28 AA;

  Query Match 4.2%; Score 7; DB 2; Length 28;
  Best Local Similarity 100.0%; Pred. No. 13;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 HTRTHTG 115
        |||||||
Db 19 HTRTHTG 25

SEQ ID NO: 5

RESULT 7
I66494/c
LOCUS I66494 7218 bp DNA linear PAT 28-DEC-1997
DEFINITION Sequence 14 from patent US 5670367.
ACCESSION I66494
VERSION I66494.1 GI:2724471
KEYWORDS .
SOURCE Unknown.
  ORGANISM Unknown.
  Unclassified.
REFERENCE 1 (bases 1 to 7218)
  AUTHORS Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
  TITLE Recombinant fowlpox virus
  JOURNAL Patent: US 5670367-A 14 23-SEP-1997;
FEATURES Location/Qualifiers
  source 1. .7218
  /organism="unknown"
  /mol_type="unassigned DNA"
ORIGIN

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  Query Match             5.5%;  Score 72;  DB 6;  Length 7218;
  Best Local Similarity   8.3%;  Pred. No. 3.7e-10;
  Matches   33;  Conservative  214;  Mismatches  149;  Indels    0;  Gaps    0;

Qy        911 ACAGTGCAACAAGTCAGGAGACCTAGGTCCTACTCCTGACACTTGCTAATTAGCTCTATG 970
              | |  |||   || ||  |     |   ||||    ||  | | | |||  || |  | |
Db       1504 AAACGGCATGTAGGCATCACTGTAATTACCTATCTATGCAAGTAGTTAAAGAGATAGAAG 1445

Qy        971 ACTCTGGGCAAATCGCATATCTGGGCCTCAGTTTCCTCATCTGTAAAAATGACAGCAAAC 1030
              | | |||   ::  : : :   :::    ::       :   : ::::: :: :: :::
Db       1444 AATTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1385

Qy       1031 TCGTAATGCTCAATAAATGTTTAAATAACAACTGAAAAGAAAGAAACCAAGTCAGGCGAC 1090
               : :: :   :: ::: :   ::: :: ::  :::::::::::::  :::  ::: ::
Db       1384 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1325

Qy       1091 AAGGAGCGTAGAACAGACCAAACGAGGCGGCCGCCGAAGGAGACGGAAGCCAGGTGTGGG 1150
              :::::: : :::: :::  ::: :::: ::  :  :::::::: :::::  ::: : :::
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Qy       1151 CGAGGAGTAAGAAGAGGGGGCGCGCAGCCCGAAATAAGGGTTGCAGGACCAGCGACCGAG 1210
               :::::: :::::::::::: : : ::   :::: :::::  : ::::  :: ::  :::
Db       1264 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1205

Qy       1211 AGATAGATATACAGAGAGCCGGAGCGAAGAGCACGCGAGCACACAGCCTCCGCTCCAGCC 1270
              ::: ::: : : ::::::  :::: :::::: : : ::: : : ::     :    ::
Db       1204 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1145

Qy       1271 GAAGAGAGGGCAGCTAACAAGAAGAAACGCAGATGA 1306
              :::::::::: ::  :: ::::::::: : ::: ::
Db       1144 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1109
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RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
```

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;       TELEFAX:  (703)683-4109
;       TELEX:  899149
;   INFORMATION FOR SEQ ID NO:  14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  7218 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     IMMEDIATE SOURCE:
;       CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             5.5%;  Score 72;  DB 1;  Length 7218;
  Best Local Similarity   8.3%;  Pred. No. 9.7e-12;
  Matches   33;  Conservative  214;  Mismatches  149;  Indels    0;  Gaps    0;

Qy        911 ACAGTGCAACAAGTCAGGAGACCTAGGTCCTACTCCTGACACTTGCTAATTAGCTCTATG 970
              | |  |||   || ||  |     |   ||||    ||  | | | |||  || |  | |
Db       1504 AAACGGCATGTAGGCATCACTGTAATTACCTATCTATGCAAGTAGTTAAAGAGATAGAAG 1445

Qy        971 ACTCTGGGCAAATCGCATATCTGGGCCTCAGTTTCCTCATCTGTAAAAATGACAGCAAAC 1030
              | | |||   ::  : : :   :::    ::       :   : ::::: :: :: :::
Db       1444 AATTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1385

Qy       1031 TCGTAATGCTCAATAAATGTTTAAATAACAACTGAAAAGAAAGAAACCAAGTCAGGCGAC 1090
               : :: :   :: ::: :   ::: :: ::  :::::::::::::  :::  ::: ::
Db       1384 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1325

Qy       1091 AAGGAGCGTAGAACAGACCAAACGAGGCGGCCGCCGAAGGAGACGGAAGCCAGGTGTGGG 1150
              :::::: : :::: :::  ::: :::: ::  :  :::::::: :::::  ::: : :::
Db       1324 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1265

Qy       1151 CGAGGAGTAAGAAGAGGGGGCGCGCAGCCCGAAATAAGGGTTGCAGGACCAGCGACCGAG 1210
               :::::: :::::::::::: : : ::   :::: :::::  : ::::  :: ::  :::
Db       1264 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1205

Qy       1211 AGATAGATATACAGAGAGCCGGAGCGAAGAGCACGCGAGCACACAGCCTCCGCTCCAGCC 1270
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Db       1204 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1145

Qy       1271 GAAGAGAGGGCAGCTAACAAGAAGAAACGCAGATGA 1306
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